

AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions, and listings, of claims in the application.

Listing of Claims:

Claims 1-8 (cancel without prejudice or disclaimer).

Claim 9 (currently amended). A host cell which produces a modified DNA polymerase having ~~[[an]] the amino acid sequence that shares not less than 95% homology to~~ of SEQ ID NO:4, ~~which DNA polymerase during DNA sequencing effectively incorporated fluorescent dye-labeled dideoxynucleotide terminators ddCTP, ddATP, ddTTP and ddGTP, and has a reduction in the selective discrimination against incorporation of fluorescent dye-labeled dideoxynucleotide terminators ddCTP and ddATP,~~

~~wherein the DNA polymerase in its unmodified state has leucine, glutamate, and glutamate residues at positions 342-344, respectively, and a phenylalanine at position 422, the positions being determined based on a last lysine residue in the end of the sequence counted as position 588, wherein the DNA polymerase selectively discriminates against incorporation of fluorescent dye-labeled dideoxynucleotide terminators ddCTP and ddATP but does not discriminate against incorporation of fluorescent dye-labeled dideoxynucleotide terminators ddTTP and ddGTP.~~

Claim 10 (original). The host cell according to claim 9, wherein the modified DNA polymerase has proofreading 3'-5' exonuclease activity during DNA sequencing of a DNA strand from a template, such that the DNA polymerase functions to excise mismatched nucleotides from the 3' terminus of the DNA strand at a faster rate than the rate at which the DNA polymerase functions to remove nucleotides matched correctly with nucleotides of the template.

Claim 11 (cancel without prejudice or disclaimer).

Claim 12 (original). The host cell according to claim 9, wherein the DNA polymerase is encoded by nucleotide sequence SEQ IDS NO:3.

Claim 13 (original). The host cell of claim 9, which is E. coli.

Claims 14-28 (cancel without prejudice or disclaimer).

Claim 29. (Amended) A DNA construct comprising:

- (i) a nucleotide sequence encoding a modified DNA polymerase which has an amino acid sequence that shares not less than 95% homology to a ~~DNA polymerase isolated from a strain of *Bacillus stearothermophilus* of *Bacillus caldotenax*, having an amino acid sequence that shares not less than 95% homology to~~ SEQ ID NO:4, ~~which~~ wherein said nucleotide sequence encodes threonine, proline and leucine ~~residues~~ at positions corresponding to positions 342-344, respectively, and a tyrosine ~~residue~~ at a position corresponding to position 422, wherein the DNA polymerase in its unmodified state has leucine, glutamate, and glutamate ~~residues~~ at positions 342-344, respectively, and a phenylalanine at position 422, the positions being determined based on a last lysine residue in the end of the sequence counted as position 588; and
- (ii) a vector, for introducing the DNA construct into eukaryotic and procaryotic host cells.

Claim 30 (original). The DNA construct according to claim 29 wherein the vector is a cloning vector or an expression vector.

Claims 31-38 (cancel without prejudice or disclaimer).

Claim 39. (Amended) A modified nucleotide sequence encoding a DNA polymerase which has an amino acid sequence that shares not less than 95% homology to a ~~DNA~~

~~polymerase isolated from a strain of *Bacillus stearothermophilus* of *Bacillus caldotenax*,
having an amino acid sequence that shares not less than 95% homology to SEQ ID NO:4,
which wherein said~~ nucleotide sequence encodes threonine, proline and leucine ~~residues~~
at positions corresponding to positions 342-344, respectively, and a tyrosine ~~residue~~ at a
position corresponding to position 422, wherein the DNA polymerase in its unmodified
state has leucine, glutamate, and glutamate ~~residues~~ at positions 342-344, respectively,
and a phenylalanine at position 422, the positions being determined based on a last lysine
residue in the end of the sequence counted as position 588.

Claim 40. (previously amended) The modified nucleotide sequence according to claim
39 which has the nucleotide sequence of SEQ ID NO:3.

Claims 41-56 (cancel without prejudice or disclaimer).